



_	-	-	_						_	gat Asp				_		384
										acc Thr						432
_		_					_	_		gcc Ala 155					_	480
										ttg Leu						528
										tcg Ser						576
										ccg Pro						624
		Gln	Ile	Tyr	Ala	Val	Glu	Gly	Gly	tgc Cys	Tyr					672
_				_	_		_		_	gta Val 235		_		_		720
gac Asp	aag Lys	gag Glu	atg Met	ttc Phe 245	ctc Leu	aag Lys	gcc Ala	ggc Gly	ggc Gly 250	ggt Gly	ttt Phe	gcc Ala	atg Met	att Ile 255	ttc Phe	768
										ctc Leu						816
										atg Met						864
-							_			cgg Arg			_	_		912
										gtc Val 315						960
										gac Asp						1008
	gtg Val		_	_	_	_	_		cag Gln	tag						1041

<210> 2 <211> 346 <212> PRT

<213> Unknown Organism <223> Description of Unknown Organism: Obtained from an environmental sample

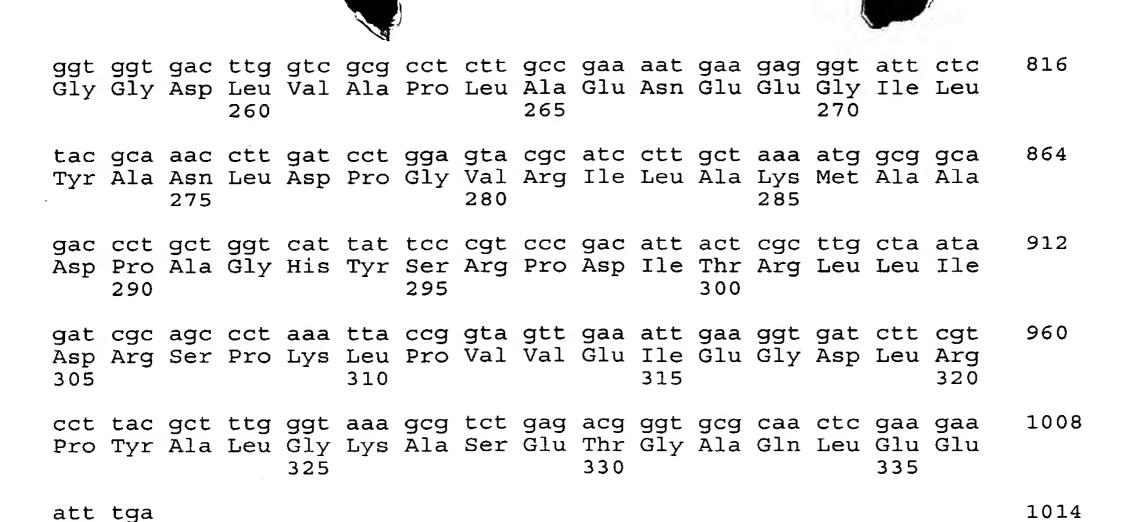
<400> 2 Met Ser Glu Pro Met Thr Lys Tyr Arg Gly Ala Ala Val Gln Ala Ala Pro Val Phe Leu Asp Leu Asp Arg Thr Val Glu Lys Ala Ile Gly Leu Ile Glu Gln Ala Ala Lys Gln Asp Val Arg Leu Ile Ala Phe Pro Glu Thr Trp Ile Pro Gly Tyr Pro Phe Trp Ile Trp Leu Gly Ala Pro Ala Trp Gly Met Arg Phe Val Gln Arg Tyr Phe Glu Asn Ser Leu Val Arg 70 Gly Ser Lys Gln Trp Gln Ala Leu Ala Asp Ala Ala Arg Arg His Gly Met His Val Val Ala Gly Tyr Ser Glu Arg Ala Gly Gly Ser Leu Tyr 105 Met Gly Gln Alà Ile Phe Gly Pro Asp Gly Asp Leu Ile Ala Ala Arg ·120 Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly Glu Gly 135 Asp Gly Ser His Leu Ala Val His Asp Thr Ala Ile Gly Arg Leu Gly 145 Ala Leu Cys Cys Trp Glu His Ile Gln Pro Leu Ser Lys Tyr Ala Met 170 Tyr Ala Ala Asp Glu Gln Val His Val Ala Ser Trp Pro Ser Phe Ser 185 180 Leu Tyr Arg Gly Met Ala Tyr Ala Leu Gly Pro Glu Val Asn Thr Ala 200 Ala Ser Gln Ile Tyr Ala Val Glu Gly Gly Cys Tyr Val Leu Ala Ser 215 210 Cys Ala Thr Val Ser Pro Glu Met Ile Lys Val Leu Val Asp Thr Pro 235 230 Asp Lys Glu Met Phe Leu Lys Ala Gly Gly Phe Ala Met Ile Phe Gly Pro Asp Gly Arg Ala Leu Ala Glu Pro Leu Pro Glu Thr Glu Glu 270 265 260 Gly Leu Leu Val Ala Asp Ile Asp Leu Gly Met Ile Ala Leu Ala Lys 280 Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr Arg 300 295 290 Leu Leu Leu Asp Arg Pro Ala Gln Arg Val Val Thr Leu Asp Ala 315 310 Ala Phe Glu Pro Gln Asn Glu Asp Lys Gly Asp Ala Pro Ala Leu Arg 335 325 330 Val Val Ala Glu Ser Ala Ala Ala Gln 340

```
<210> 3
<211> 1014
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Obtained from an environmental sample

<220>
<221> CDS
<222> (1)..(1014)
```

atg														atc Ile 15		48
														gaa Glu		96
														tgg Trp		144
									_					gca Ala		192
		_	_							_		_	_	ggc Gly		240
	_	_	_			_		_	_		_			atg Met 95	_	288
														agt Ser		336
				_			_				_		_	aag Lys		384
				_	_	_		_			_		_	ggt Gly	tca Ser	432
_	Leu		_					_			_			tta Leu		480
_		_				_					-	_		gca Ala 175		528
				His										tat Tyr		576
														tct Ser		624
		_	_	_			_							gcg Ala		672
_				_		_	_		_		_	_	_	aag Lys		720
														cct Pro 255		768



<210> 4

Ile

<211> 337

<212> PRT

<213> Unknown Organism

<223> Description of Unknown Organism: Obtained from an environmental sample

<400> 4 Met Lys Glu Ala Ile Lys Val Ala Cys Val Gln Ala Ala Pro Ile Tyr 10 Met Asp Leu Glu Ala Thr Val Asp Lys Thr Ile Glu Leu Met Glu Glu Ala Ala Arg Asn Asn Ala Arg Leu Ile Ala Phe Pro Glu Thr Trp Ile Pro Gly Tyr Pro Trp Phe Leu Trp Leu Asp Ser Pro Ala Trp Ala Met Gln Phe Val Arg Gln Tyr His Glu Asn Ser Leu Glu Leu Asp Gly Pro 70 65 Gln Ala Lys Arq Ile Ser Asp Ala Ala Lys Arg Leu Gly Ile Met Val Thr Leu Gly Met Ser Glu Arg Val Gly Gly Thr Leu Tyr Ile Ser Gln 100 105 110 Trp Phe Ile Gly Asp Asn Gly Asp Thr Ile Gly Ala Arg Arg Lys Leu Lys Pro Thr Phe Val Glu Arg Thr Leu Phe Gly Glu Gly Asp Gly Ser 135 Ser Leu Ala Val Phe Glu Thr Ser Val Gly Arg Leu Gly Gly Leu Cys 150 145 155 Cys Trp Glu His Leu Gln Pro Leu Thr Lys Tyr Ala Leu Tyr Ala Gln 165 170 Asn Glu Glu Ile His Cys Ala Ala Trp Pro Ser Phe Ser Leu Tyr Pro 180 185 190 Asn Ala Ala Lys Ala Leu Gly Pro Asp Val Asn Val Ala Ala Ser Arg Ile Tyr Ala Val Glu Gly Gln Cys Phe Val Leu Ala Ser Cys Ala Leu 215 220 210 Val Ser Gln Ser Met Ile Asp Met Leu Cys Thr Asp Asp Glu Lys His 230 235 Ala Leu Leu Leu Ala Gly Gly Gly His Ser Arg Ile Ile Gly Pro Asp 250 Gly Gly Asp Leu Val Ala Pro Leu Ala Glu Asn Glu Glu Gly Ile Leu

Tyr Ala Asn Leu Asp Pro Gly Val Arg Ile Leu Ala Lys Met Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Ile Thr Arg Leu Leu Ile Asp Arg Ser Pro Lys Leu Pro Val Val Glu Ile Glu Gly Asp Leu Arg Pro Tyr Ala Leu Gly Lys Ala Ser Glu Thr Gly Ala Gln Leu Glu Glu Ile

